

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 7, 2002, 10:03:24 ; Search time 15.5455 Seconds
(without alignments)
3931.234 Million cell updates/sec

Title: US-09-125-005-6
Perfect score: 3384
Sequence: 1 MAQSTATSPGGTTFEHLMS.....PCKARKQPIKEETFEAIH 636

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71.*

- 1: pir1.*
- 2: pir2.*
- 3: pir3.*
- 4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	851.5	25.2	395	JH0631	cellular tumor ant
2	778	23.0	367	S02193	cellular tumor ant
3	760.5	22.5	386	S51648	cellular tumor ant
4	749	22.1	396	JH0633	cellular tumor ant
5	741.5	21.9	393	JC6176	tumor suppressor p
6	741	21.9	363	A29376	cellular tumor ant
7	735.5	21.7	391	S02192	cellular tumor ant
8	724.5	21.4	391	JC6193	tumor suppressor p
9	724.5	21.4	393	DNH053	cellular tumor ant
10	718.5	21.2	393	S06594	cellular tumor ant
11	711.5	21.0	390	DNM553	cellular tumor ant
12	702	20.7	381	S38824	cellular tumor ant
13	248.5	7.3	77	I46226	cellular tumor ant
14	151.5	4.5	903	T00074	hypothetical prote
15	148.5	4.4	925	T19361	hypothetical prote
16	145	4.3	864	T85335	hypothetical prote
17	145	4.3	864	T04518	hypothetical prote
18	143	4.2	1819	T32008	hypothetical prote
19	142	4.2	964	T41547	hypothetical prote
20	139.5	4.1	1221	T13283	probable transcrip
21	133	3.9	1273	S58782	SEG31 protein - ye
22	131.5	3.9	2364	A56577	microtubule-associ
23	130.5	3.9	1026	T20369	hypothetical prote
24	129	3.8	306	A24354	extensin precursor
25	128	3.8	1241	T18311	hypothetical prote
26	127.5	3.8	784	S26638	SPR-1 protein - hu
27	127	3.8	3938	T42761	Bassoon protein -
28	126	3.7	817	S51342	verprolin - yeast
29	126	3.7	1791	T02909	hypothetical prote

ALIGNMENTS

RESULT 1

JH0631
cellular tumor antigen p53 - rainbow trout
C:Species: Oncorhynchus mykiss (rainbow trout)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: JH0631
R:de Fromental, C.C.; Pakdel, F.; Chapus, A.; Baney, C.; May, P.; Soussi, T.
Gene 112, 241-245, 1992
A:Title: Rainbow trout p53: cDNA cloning and biochemical characterization.
A:Reference number: JH0631; MUID:92210006
A:Accession: JH0631
A:Molecule type: mRNA
A:Residues: 1-396 <DEF>
A:CROSS-references: GB:M75145; NID:g213828; PIDN:AAA49605.1; PID:g213829
A:Experimental source: liver
C:Comment: This protein is the product of a tumor suppressor gene, p53, whose inacti
C:Superfamily: cellular tumor antigen p53
C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; ph
F:164,167,227,231/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
F:395/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match 25.2%; Score 851.5; DB 1; Length 396;
Best Local Similarity 55.68; Pred. No. 1.3e-51;
Matches 170; Conservative 43; Mismatches 86; Indels 7; Gaps 5;

Qy	93	VPHSPYAQS-STFDTMS-PAPVIPSNTDYPGPHFEVTFQOSAKSATWYSPLLKK	150
Db	61	VSATEPAPQPSITLDTGSPPTSTVPTTSDYVGALGFQALFLOSSTAKSVTCYSPDLNK	120
Qy	151	LYCOIAKTCPIQIKVSTPPPGCTATAMPVYKKAHVTDVVKCPNHELGRDPNEQSAP	210
Db	121	LFCOLAKTCPIQIVVDHPPPGAVVRAIYKLSADVVRCPHQSSENEG-PAP	179
Qy	211	ASHLIVEGNNSLQVYDVPVGTGRQSVVYVPEPPQGVTEFTILYNFMCNSSCVGGMNRRP	270
Db	180	RGLVLRVEGNQRSEYMEDGNTLRHSLVYVPEPPQGVTEFTILYNFMCNSSCVGGMNRRP	239
Qy	271	ILITILEMRDQVIGRRSFEGRICACPRGRKADEHYREQQALN-ESSAKNGAASKRA	329
Db	240	ILITITLETQEQQLIGRRSFVRVACPCFRGRKTEENLKKQOETTLETETKPAQGIKRA	299
Qy	330	FKOSPPAVPALGAGVKKRRH---GDEPTYLQVGRGNFEILMKLESLELMELVPOPLV	386
Db	300	MKEASLPAPQPGASKTKTSSPAVSDEITYLQIRGKEYEMLKFNDSLSLSLVPVADA	359
Qy	387	DSYRQQ	392
Db	360	DYRQK	365

RESULT 2

S02193

Best Local Similarity 44.28; Pred. No. 2.7e-45;
Matches 169; Conservative 63; Mismatches 105; Indels 45; Gaps 11;

```
QY 60 SYMAQFNLLSSMTDMQSSRAASAGPYT-----PEHAASVPTHS-PYAQPSSSTDTM 109
Db 24 NLLPENLLSS---ELSAVDLLPYTDVATWLDCEPNEAQPPEPSAPAAPPAT---- 76

QY 110 SAPV-----IPSTNDYGPPIHFVFTQOSTAKSATWTYSPLLKKLYQIAKTCP 161
Db 77 -PAPATSWPLSSFVSQTYTGNFYGRFLGQSTAKSVCTYSPSLNKLFCOLAKTCPV 135

QY 162 QIKVSTPPPGGTAIRAMPVYKKAETHVTDVVKRCNHHGLDFENEGOSAPASHLIRVEGNN 221
Db 136 QLVWDSPPPGGTRVAMAIYKKLEHTEVVRCHPHHSSSDYSDG-IAPQPHLIRVEG 194

QY 222 LSOYVDVDPVTGRQSVVVPYEPQVQTEFTTILYNFMCNSCVGGMNRRPILIIITLEM 281
Db 195 RAEYLDNRNTRFHSVVVPYSPESIDSECTTHYNFMCNSCMGCMGNRRPILITILED 254

QY 282 GOVLGRRRFEGRICACGRDKADEHYREQ-QALNESSAKNGAASKRAFQSPVAPVAL 340
Db 255 GMLLRNSSFVEVACVACQGRDARTENLRKKQSGCPEPPR---STKRALPTNTSSPQ- 310

QY 341 GAGVKRRRGDDTYLQVGRGNFEILMKLKSLELMELVPOPLVDYSYRQOQOQLQRPS 400
Db 311 ----PKKKPLDCEYFTLQIRGFKRYEMPRELNDALLEKDAL-----DGREP 360

QY 401 HLQP---PSYGPVLSPMNKVVHG 419
Db 361 HLKSKRPSPSCHKKPKMLKREG 382

RESULT 4
JH0633
cellular tumor antigen p53 - golden hamster
N;Alternate names: tumor-suppressor protein p53
C;Species: Mesocricetus auratus (golden hamster)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: JH0633
R;Legros, Y.; McIntyre, P.; Soussi, T.
Gene 112, 247-250, 1992.
A;Title: The cDNA cloning and immunological characterization of hamster p53.
A;Reference number: JH0633; MUID:92210007
A;Accession: JH0633
A;Molecule type: mRNA
A;Residues: 1-396 <LEG>
A;Cross-references: GB:M75144; NID:g191414; PID:AAA37085.1; PID:g191415
A;Experimental source: kidney, strain Mp1
C;Genetics:
```

C;Superfamily: cellular tumor antigen p53
C;Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; ph
F;179,182,241,745/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
F;395/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match 22.1% ; Score 749; DB 1; Length 396;
Best Local Similarity 43.8%; Pred. No. 1.7e-44;
Matches 165; Conservative 58; Mismatches 104; Indels 50; Gaps 10;

QY 14 TTEHLWSSLEPDSVTFDLPQSGRGNVEVGGTSDSSMDVFHELGMTTSVMAQFNLLSSTD 73
 | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
Db 18 TFSDLKLLPPNNVLSTLPSS-----DSIEELFLENVA-----CWLEDPGE 59

QY 74 QMSRRASASPTPEHAASVP---THSPYAOPSTFTDTMSPAPV---IPNSTDPGPHHF 127
 | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
Db 60 ALQGSAAAAAAPA--AAEDPVAETPAVASAPAT----PWPLSSSVPSKYTYQGDYGF 112

QY 128 EYTFQOSTAKSATWTYSPLLKKLYCQIAKCTPIKVSTPPPPGTAIRAMPYVKAHV 187
 : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
Db 113 RGFLHSGTAKSVTCTYSPSLNKLFCOLAKTCPQLWSVSTPPPGTRVRMATYKKLOYM 172

QY 188 TDVKRKCPNHGLGRDFNGOS--APASHLIRVEGHNLISOYDDDPVTGROSVVVPEYPPOVG 246
 : : : : : | : : : : : | : : : : : | : : : : : | : : : : :

R;Soussi, T.; de Fromental, C.C.; Breugnot, C.; May, E.
Nucleic Acids Res. 16, 11384, 1988
A:Title: Nucleotide sequence of a cDNA encoding the rat p53 nuclear oncoprotein.
C:Reference number: S02192; MUID:89083585
A:Accession: S02192

A:Molecule type: mRNA
A:Residues: 1-391 <SOU>
A:Cross-references: EMBL:X13058; NID:956828; PIDN:CAA31457.1; PID:956829
R;Hulla, J.E.; Schneider, R.P.
Nucleic Acids Res. 21, 713-717, 1993
A:Title: Structure of the rat p53 tumor suppressor gene.
C:Reference number: S41149; MUID:93181268
A:Accession: S41149

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA
A:Residues: 1-173, 'W', 175-391 <HUL>
A:Cross-references: EMBL:L07909
A:Note: The nucleotide sequence was submitted to the EMBL Data Library, December 1992
C:Genetics:

A:Introns: 25/2; 32/3; 123/3; 185/1; 259/2; 305/1; 329/3; 365/2
C:Superfamily: cellular tumor antigen p53
C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; phospho
F:174,177,236,240/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
F:390/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match 21.7%; Score 735.5; DB 1; Length 391;
Best Local Similarity 42.8%; Pred. No. 1.5e-43;
Matches 167; Conservative 55; Mismatches 87; Indels 81; Gaps 12;

QY 14 TFEHLNLSLEPDTYDLPQSSRGNNVGGTSSMDVYF-----HLEGMTTSVMAQFN 66

Db 18 TFCWKLPPDDI---LPTA-----TGSPNSMEDLFPQDVAALEGG----- 58

QY 67 LLSTMDQMSRAASPYTPPEHAASVTPHSAQPSSTFTDMSAPV----- 114

Db 59 -----PEALQV--SAPAAQEPG--TEAPAPVAPASATPWPLSS 93

QY 115 -IPNTDYPGPHFETVFOQSTAKSATWYTSPLKLYCQIAKTCPIQIKVSTPPPGT 173

Db 94 SVPSQKTYQNGYFHLGFLQSTAKSVMTYISLKLFCOLAKTCVQLWVSTPPGT 153

QY 174 AIRAMPYKKAHVTDVWRCNPNHGLGRDFNEGQSPASHLIRVEGNLSQYVDDPVTGR 233

Db 154 RVRAMAIYKKSQHTVEVRCPPHERCSD-GDG-LAPPQHLIRVEGNFYAEYLDROTFR 211

QY 234 QSVVYPPQVGTETTYLYNFMNSCGVGMNRRPILITILEMDRGVGLGRSFEGR 293

Db 212 HSNVYPPPEVGSYDTHYKIMNSCGMGNRRPILITILEMDRGVGLGRSFEGR 271

QY 294 ICACPGRRDKADHDHYEQO-----ALNESSAKNGAASKRAFKQSPAPVAPALGAGVKKRH 349

Db 272 VCACPGRRDTEENRKEEHCPELPGSA-----KRALPTSTSSPO-----QKKP 320

QY 350 GDETYLYVGRNFEILMKLESLEME 379

Db 321 LDGEYFTKIRGRFENFRELNEALEKD 350

RESULT 8

JC6193

tumor suppressor p53 - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change 20-Jun-2000
C:Accession: JC6193

Gene 185, 169-173, 1997
R;Le Goas, F.; May, P.; Ronco, P.; de Fromental, C.C.

A:Title: cDNA cloning and immunological characterization of rabbit p53.
A:Reference number: JC6193; MUID:97208669

A:Accession: JC6193

A:Molecule type: mRNA

A:Residues: 1-391 <LEA>

A:Cross-references: EMBL:X90592; NID:g1532043; PIDN:CAA62216.1; PID:g1532044

C:Genetics:

A:Gene: p53
C:Superfamily: cellular tumor antigen p53
C:Keywords: tumor

Query Match 21.4%; Score 724.5; DB 2; Length 391;
Best Local Similarity 43.5%; Pred. No. 8.6e-43;
Matches 165; Conservative 54; Mismatches 103; Indels 57; Gaps 10;

QY 21 SLEP---DSYFQDLPQSSRGNNVGGTSSMDVHLEGMTTSVMAQFNLLSSMTDQMS 77

Db 9 SLEPPLSQEFTFSLKLLPENL-----LTSLNPPVDDLLSLED----- 48

QY 78 RAASAPYTPPEHAASVTP-THSPYAPQSPSTFTDMSAPV-----IPSTNDYFGPHFE 128

Db 49 -VANWLNEDPEGLRYPAPAPAPAPAPAPAPATSNPLSSSVPSQRTYHGTGFR 107

QY 129 VTQQSTAKSATWYTSPLKLYCQIAKTCPIQIKVSTPPPGTAIRAMPYKKAHV 188

Db 108 LGFLHSGTAKSVTCTYSPCLNKLFCOLAKTCVQLWVSTPPGTRVRAMAIYKKSQHT 167

QY 189 DVYKRCNPNHGLGRDFNEGQSPASHLIRVEGNLSQYVDDPVTGRQSVVYPPQVGT 248

Db 168 EVVRCPPHERCSD-SDG-LAPPQHLIRVEGNLRAEYLDROTFRHSVYVYPPPEVGS 225

QY 249 FTYLYNFMNSCGVGMNRRPILITILEMDRGVGLGRSFEGRICACPGRRDKADEH 308

Db 226 CTHIYNYMNSCGMGNRRPILITILEMDRGVGLGRSFEGRICACPGRRDRTEEN 285

QY 309 YRQOALNESSAKNG-----AASKRAFKQSPAPVAPALGAGVKKRHGEDTYLYQVR 360

Db 286 FR-----KKGPCPELPGSSKRAL-----PTTTDSSPQTKKPLDGEYFILKIR 331

QY 361 GRENFEILMKLESLEME 379

Db 332 GREFEFRELNEALEKD 350

RESULT 9

DNH053

cellular tumor antigen p53 [validated] - human

N:Alternate names: cellular phosphoprotein p53; oncoprotein p53; transformation sup

C:Species: Homo sapiens (man)

C:Date: 05-Oct-1988 #sequence_revision 18-Nov-1994 #text_change 15-Sep-2000

C:Accession: A25224; A43073; J0436; S40773; S42669; A25397; B25397;

4903; 158354; 178850; 152681; S60153

R;Lamb, P.; Crawford, L.
Mol. Cell. Biol. 6, 1379-1385, 1986

A:Title: Characterization of the human p53 gene.

A:Reference number: A25224; MUID:87064416

A:Accession: A25224

A:Molecule type: DNA

A:Residues: 1-393 <LAMB>

A:Cross-references: EMBL:X01405; GB:M13121; GB:N00032; NID:g189460; PIDN:AAAS9987.1;

R;Buchman, V.L.; Chumakov, P.M.; Ninkina, N.N.; Samarina, O.P.; Georgiev, G.P.

Gene 70, 245-252, 1988

A:Title: A variation in the structure of the protein-coding region of the human p53

A:Reference number: J0436; MUID:89108008

A:Accession: A43073

A:Molecule type: DNA

A:Residues: 1-393 <BUCL>

A:Cross-references: EMBL:M22898; NID:g189474

A:Note: this 72-Arg allele appears to be about 5 times more frequent than the 72-Pro

A:Accession: J0436

A:Molecule type: DNA

A:Residues: 1-71, 'P', 73-393 <BUC2>

A:Cross-references: EMBL:M22898; NID:g189474; PIDN:AAAS9988.1; PID:g189476

R;Chumakov, P.M.; Almazov, V.P.; Jenkins, J.R.

submitted to the EMBL Data Library, August 1990.

A:Reference number: S40773

A:Accession: S40773

A:Molecule type: DNA

A:Residues: 1-393 <CHUD>

A:Cross-references: EMBL:X54156; NID:g35213; PIDN:CAA38095.1; PID:g35214
 R:Matlashewski, G.; Lamb, P.; Pin, D.; Peacock, J.; Crawford, L.; Benchimol, S.
 EMBO J. 3, 3257-3262, 1984
 A:Title: Isolation and characterization of a human p53 cDNA clone: expression of the human p53 protein in COS cells.
 A:Reference number: S42669; MUID:85126934
 A:Accession: S42669
 A:Molecule type: mRNA
 A:Residues: 101-393 <MK1>
 A:Cross-references: EMBL:X01405; NID:g35215; PIDN:CAA25652.1; PID:g642241
 R:Zakut-Houri, R.; Blenz-Tadmor, B.; Givol, D.; Oren, M.
 EMBO J. 4, 1251-1255, 1985
 A:Title: Human p53 cellular tumor antigen: cDNA sequence and expression in COS cells.
 A:Reference number: A22837; MUID:85230577
 A:Accession: A22837
 A:Molecule type: mRNA
 A:Residues: 1-71, 'P', 73-393 <2AK>
 A:Cross-references: EMBL:X02469; EMBL:M60950; NID:g35209; PIDN:CAA26306.1; PID:g35210
 R:Harlow, E.; Williamson, N.M.; Ralston, R.; Hellman, D.M.; Adams, T.E.
 Mol. Cell. Biol. 5, 1601-1610, 1985
 A:Title: Molecular cloning and in vitro expression of a cDNA clone for human cellular tumor antigen p53.
 A:Reference number: A55060; MUID:85267676
 A:Accession: A55060
 A:Molecule type: mRNA
 A:Residues: 1-71, 'P', 73-272, 'H', 274-393 <HAR>
 A:Cross-references: GB:X03199; NID:g189478; PIDN:AAA59989.1; PID:g189479
 A:Experimental source: clone pR4-2, cell line A431
 R:Haris, N.; Brill, E.; Shohat, O.; Prokocimer, M.; Wolf, D.; Arai, N.; Rotter, V.
 Mol. Cell. Biol. 6, 4650-4656, 1986
 A:Title: Molecular basis for heterogeneity of the human p53 protein.
 A:Reference number: A93086; MUID:87089826
 A:Accession: A25397
 A:Molecule type: mRNA
 A:Residues: 1-78, 'T', 80-393 <HAR>
 A:Cross-references: EMBL:M14694; NID:g339813; PIDN:AAA61211.1; PID:g339814
 A:Experimental source: clone p53-H-1, transformed hybridoma SV-80 cell line
 A:Accession: B25397
 A:Molecule type: mRNA
 A:Residues: 1-71, 'P', 73-78, 'T', 80-393 <HAR2>
 A:Cross-references: EMBL:M14695; NID:g339815; PIDN:AAA61212.1; PID:g339816
 A:Experimental source: clone p53-H-19, transformed hybridoma SV-80 cell line
 R:Matlashewski, G.J.; Tuck, S.; Pim, D.; Lamb, P.; Schneider, J.; Crawford, L.V.
 Mol. Cell. Biol. 7, 961-963, 1987
 A:Title: Primary structure polymorphism at amino acid residue 72 of human p53.
 A:Reference number: S42452; MUID:87144273
 A:Accession: S42452
 A:Molecule type: mRNA; DNA
 A:Residues: 66-71, 'P', 73-79 <MK12>
 A:Experimental source: clone lambda C113
 A:Note: 72-Cys was also found, and appears to represent a polymorphism
 A:Accession: S42453
 A:Molecule type: mRNA; DNA
 A:Residues: 66-79 <MK13>
 A:Experimental source: clone J6K
 R:Farrell, P.J.; Allan, G.J.; Shanahan, F.; Vousden, K.H.; Crook, T.
 EMBO J. 10, 2879-2887, 1991
 A:Title: p53 is frequently mutated in Burkitt's lymphoma cell lines.
 A:Reference number: I38082; MUID:92007731
 A:Accession: I38082
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-189, 'L', 190-393 <F01>
 A:Cross-references: EMBL:X60010; NID:g506432; PIDN:CAA42625.1; PID:g506433
 A:Note: deletion of a C nucleotide causes a frameshift at position 566
 A:Accession: I38083
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-192, 'R', 194-393 <F02>
 A:Cross-references: EMBL:X60011; NID:g506434; PIDN:CAA42626.1; PID:g506435
 A:Accession: I38084
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-393 <F03>
 A:Cross-references: EMBL:X60012; NID:g506436; PIDN:CAA42627.1; PID:g506437

A:Accession: I38085
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-245, 'T', 247-393 <F04>
 A:Cross-references: EMBL:X60013; NID:g506438; PIDN:CAA42628.1; PID:g506443
 A:Accession: I38086
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-236, 'I', 238-393 <F05>
 A:Cross-references: EMBL:X60014; NID:g506440; PIDN:CAA42629.1; PID:g506441
 A:Accession: I38087
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-247, 'Q', 249-393 <F06>
 A:Cross-references: EMBL:X60015; NID:g506442; PIDN:CAA42630.1; PID:g506443
 A:Accession: I38088
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-71, 'P', 73-237, 'Y', 239-393 <F07>
 A:Cross-references: EMBL:X60016; NID:g506444; PIDN:CAA42631.1; PID:g506445
 A:Accession: I38089
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-247, 'Q', 249-393 <F08>
 A:Cross-references: EMBL:X60017; NID:g506446; PIDN:CAA42632.1; PID:g506447
 A:Accession: I38090
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-71, 'P', 73-162, 'H', 164-393 <F09>
 A:Cross-references: EMBL:X60018; NID:g506448; PIDN:CAA42633.1; PID:g506449
 A:Accession: I38091
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-212, 'Q', 214-393 <F10>
 A:Cross-references: EMBL:X60019; NID:g506450; PIDN:CAA42634.1; PID:g506451
 A:Accession: I38092
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-253, 'D', 255-393 <F11>
 A:Cross-references: EMBL:X60020; NID:g506452; PIDN:CAA42635.1; PID:g506453
 A:Note: all sequences submitted to the EMBL/GenBank/DBJ databases June 1991
 R:Futreal, P.A.; Barrett, J.C.; Wiseman, R.W.
 Nucleic Acids Res. 19, 5977, 1991
 A:Title: An Alu polymorphism intragenic to the TP53 gene.
 A:Reference number: I38093; MUID:92107726
 A:Accession: I38093
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-393 <FUT>
 A:Cross-references: EMBL:X54156; NID:g35213; PIDN:CAA38095.1; PID:g35214
 R:Yamada, Y.; Yoshida, T.; Hayashi, K.; Sekiya, T.; Yokota, J.; Hirohashi, S.; Nakatani, C.
 Cancer Res. 51, 5800-5805, 1991
 A:Title: p53 gene mutations in gastric cancer metastases and in gastric cancer cell lines.
 A:Reference number: A44905; MUID:92034678
 A:Accession: A44905
 A:Molecule type: DNA
 A:Residues: 246-247, 'W', 249-250 <YAM>
 A:Cross-references: GB:S63157; NID:g37829; PIDN:AB20140.1; PID:g237830
 A:Note: sequence extracted from NCI backbone (NCBI:63157, NCBIP:63158)
 R:Hensel, C.H.; Xiang, R.H.; Sakaguchi, A.Y.; Naylor, S.L.
 Oncogene 6, 1067-1071, 1991
 A:Title: Use of the single strand conformation polymorphism technique and PCR to detect p53 mutations in gastric cancer.
 A:Reference number: I58354; MUID:91296386
 A:Accession: I58354
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 244-247, 'W', 249-252 <HEN1>
 A:Cross-references: GB:S41969; NID:g1679931; PIDN:AB19324.1; PID:g232814
 A:Accession: I78850
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 274-277, 'S', 279-282 <HEN2>

Query Match 21.2%; Score 718.5; DB 1; Length 393;
Best Local Similarity 42.1%; Pred. No. 2.3e-42;
Matches 160; Conservative 58; Mismatches 103; Indels 59; Gaps 11.

QY 14 TTEHLWSSLEPSTVFDLPSSRGNEVVGTTDSSMDVFHLEGMTTSVMAOFNLLSMTD 73
DB 18 TFSDLWLKLLPENNVLSPFSQA-----VDDL-----LSPDDLQW-LTEDGPG 60

QY 74 QMSRRAASAPVTPDEHAASVPHSPYAPQSPSTFTDMSAP-----VIPSNTDYPGPHHF 127
DB 61 DEAPRKSEAP---HMAPTPAAPTAAAP-----APAPSWPLSSSVPSOKTYHGSYGF 109

QY 128 EYTFQOSSTAKGATWTYSPLKLKLCQIAKTCPIQIKVSTPPPGTATRAMPVVYKKAHV 187
DB 110 RLGLFHSGTAKSVCTYSPDLNKKFCOLAKCPQLWDSVTPPGSRVRANAIIYKSOHM 169

QY 188 TDVYKRCPNHELGRFNEGQSPASHLLRVGNLNSQVDDPVTGROSQVVPYEPPOVGT 247
DB 170 TEVYRCPPHERCSD-SDG-LAPPOHLLRVGNLRVEYSDDRNTRFHSVWVYEPPEVGS 227

QY 248 EFTTILNPMCNSSCVGGMNRRPILIIITLEMRQDQVLGRSFEGRICACPRGRKADED 307
DB 228 DCTTHTNYMCMSCMGGMNRRPILITILEDSSGNLGRNSFEVRCVACPGRDRRTEE 287

QY 308 HYREQOALNESSAKG-----AASRAKFSQPPAVPALGAGVKKRRHGDDETYIQLV 359
DB 288 NFR-----KKGPCHELPGSTKRALPNNTSSSPQ-----PKKKPLDGEYFTLIQI 332

QY 360 RGRNFPEILMKLESLELME 379
DB 333 RGRERFEMFRELNEALKD-352

RESULT 11
DNMS53
cellular tumor antigen p53 - mouse
N:Alternate names: oncoprotein p53
C:Species: Mus musculus (house mouse)
C:Date: 28-Aug-1985 #sequence-revision 04-Oct-1996 #text-change 11-May-2000
C:Accession: A22739; S06336; A02684; S38822; S38823; S40014; I48703
R:Blenz, B.; Zakut-Houri, R.; Givol, D.; Oren, M.
EMBO J. 3, 2179-2183, 1984
A:Title: Analysis of the gene coding for the murine cellular tumour antigen p53.
A:Reference number: A22739; MUID:8502173
A:Accession: A22739
A:Molecule type: DNA
A:Residues: 1-134, 'V', 136-390 <BIE>
A:Cross-references: GB:X00876; NID:g871420; PID:g871421; GB:X01237;
R:Chumakov, P.M.
Bioorg. Khim. 13, 1691-1694, 1987
A:Title: Primary structure of DNA complementary to murine oncoprotein p53 mRNA.
A:Reference number: S06336; MUID:86221682
A:Accession: S06336
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-134, 'V', 136-390 <CHU>
R:Zakut-Houri, R.; Oren, M.; Blenz, B.; Lavie, V.; Hazum, S.; Givol, D.
Nature 306, 594-597, 1983
A:Title: A single gene and a pseudogene for the cellular tumour antigen p53.
A:Reference number: A02684; MUID:84068204
A:Accession: A02684
A:Molecule type: mRNA
A:Residues: 1-159, 'H', 161-167, 'G', 169-233, 'I', 235-390 <ZAK>
A:Cross-references: GB:X01237; GB:K01700; NID:G53575
R:Araki, N.; Nomura, D.; Yokota, K.; Wolf, D.; Brill, E.; Shohat, O.; Rotter, V.
Mol. Cell. Biol. 6, 3232-3239, 1986
A:Title: Immunologically distinct p53 molecules generated by alternative splicing.
A:Reference number: S38822; MUID:87064640
A:Accession: S38822
A:Molecule type: mRNA
A:Residues: 1-390 <ARAI>
A:Cross-references: EMBL:M13872; NID:g200198; PTDN:AAA39881.1; PID:g200199

A:Accession: S38823
 A:Molecule type: mRNA
 A:Residues: 1-167, 'G', 169-233, 'I', 235-390 <ARA2>
 A:Cross-references: EMBL:M13873
 R:Atai, N.; Nomura, D.; Yokota, K.; Wolf, D.; Brill, E.; Shohat, O.; Rotter, V.
 submitted to the EMBL Data Library, July 1988
 A:Reference number: S40014
 A:Accession: S40014
 A:Molecule type: mRNA
 A:Residues: 1-167, 'G', 169-390 <ARA3>
 A:Cross-references: EMBL:M13873; NID:g200200; PIDN:AAA39883.1; PID:g200201
 R:Jenkins, J.R.; Rudge, K.; Redmond, S.; Wade-Evans, A.
 Nucleic Acids Res. 12, 5605-5626, 1984
 A:Title: Cloning and expression analysis of full length mouse cDNA sequences encoding the
 A:Reference number: I48703; MUID:8472240
 A:Accession: I48703
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-47, 'R', 49-78, 'QW', 82-390 <RES>
 A:Cross-references: EMBL:X00741; NID:g53570; PIDN:CAA25323.1; PID:g53571
 C:Comment: This DNA-binding protein plays an essential role in the regulation of cell division.
 C:Superfamily: cellular tumor antigen p53
 C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; phosphoprotein;
 F:1-44/Domain: transcription activation #status predicted <TRA>
 F:16-26/Region: conserved region I
 F:99-289/Domain: DNA-binding core #status predicted <DBC>
 F:108-121/Region: L1 loop
 F:114-139/Region: conserved region II
 F:160-192/Region: conserved region III
 F:231-252/Region: conserved region IV
 F:233-248/Region: L3 loop
 F:267-283/Region: conserved region V
 F:313-319/Region: nuclear location signal
 F:319-357/Region: tetramer association
 F:779,12,16,23,37/Binding site: phosphate (Ser) (covalent) #status predicted
 F:173,176,235,239/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
 F:312/Binding site: phosphate (Ser) (covalent) (by cdc2 kinase) #status predicted
 F:389/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

 Query Match 21.0%; Score 711.5; DB 1; Length 390;
 Best Local Similarity 43.2%; Pred. No. 6.9e-42;
 Matches 159; Conservative 64; Mismatches 104; Indels 41; Gaps 12;

 QY 14 TFEHLWSLEPDSYFDLPQSSRGNNVGGTSSMDVHLEGMTSYMAQFNLLSSTMD 73
 DB 21 TFSGLWKLPPPE----DILSPHCHMDLLLPQD--VEEF-FEGPSEAL----- 61

 QY 74 QMSRAASAPY--TPEHAASVTHSPYAPQSPSTFTMSPAPVPSNTDYPGPHFEVTF 131
 DB 62 RVSGAPAAQDPVETPGVPAPAPA--TPW--PLSSF-----VPSQTYQNGYFHLGF 110

 QY 132 QOSSTAKSATWYSPLLKLYCQIAKTCPIQIKVSTPPPPGTAIRAMPVYKAEHVTDV 191
 DB 111 LOSGTAKSVMTYSPPLNKLFCQIAKTCPIQVQVWVATPPAGSRVRAAIYKKSQHWTEV 170

 QY 192 KRCNHELGRDFNEGQASASHLIRVEGNLSQYVDDPTGQSVVYVPEPQVGTETFT 251
 DB 171 RCPHHERCSD-GDG-LAPQHLIRVEGNLYPEYLEDROTFRHSVYVPEPEAGSEYTT 228

 QY 252 ILYNFMNCSSCGVMNRRLIITILEMRDGOVLGRSFEGRICACPGDRKADSDHYRE 311
 DB 229 IHXYMNCSSCGVMNRRLIITILEDSGNLLGRDSFEVRVCAVCPGDRKADSDHYRE 288

 QY 312 QOALNESSAKNGAASKRAFKQSPVAPVAGVYKRRHGDDETYIYQVGRNFEILMKL 371
 DB 289 KEVLCPELPPGSA--KRALPTCTASAPP-----QKKKPLDGEYFTLKIRGRKRFEMFREL 341

 QY 372 KESLELME 379
 DB 342 NEALELKD 349

RESULT 12
 S38824
 cellular tumor antigen p53, minor splice form - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
 C:Accession: S38824; S35478
 R:Atai, N.; Nomura, D.; Yokota, K.; Wolf, D.; Brill, E.; Shohat, O.; Rotter, V.
 Mol. Cell. Biol. 6, 3232-3239, 1986
 A:Title: Immunologically distinct p53 molecules generated by alternative splicing.
 A:Reference number: S38822; MUID:87064640
 A:Accession: S38824
 A:Molecule type: mRNA
 A:Residues: 1-381 <ARA>
 A:Cross-references: GB:M13874; NID:g200202; PIDN:AAA39883.1; PID:g200203
 R:Han, K.A.; Kulesz-Martin, M.F.
 Nucleic Acids Res. 20, 1979-1981, 1992
 A:Title: Alternatively spliced p53 RNA in transformed and normal cells of different
 A:Reference number: S35478; MUID:92253421
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-381 <HAN>
 A:Cross-references: EMBL:M13874; NID:g200202; PIDN:AAA39883.1; PID:g200203
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1988
 C:Comment: This sequence, produced by alternative splicing of the tenth intron, lacks
 a not known
 C:Superfamily: cellular tumor antigen p53
 C:Keywords: alternative splicing; phosphoprotein; zinc
 F:1-44/Domain: transcription activation #status predicted <TRA>
 F:16-26/Region: conserved region I
 F:99-289/Domain: DNA-binding core #status predicted <DBC>
 F:108-121/Region: L1 loop
 F:114-139/Region: conserved region II
 F:160-192/Region: conserved region III
 F:168-178/Region: conserved region IV
 F:231-252/Region: conserved region V
 F:233-248/Region: L3 loop
 F:267-283/Region: conserved region V
 F:313-319/Region: nuclear location signal
 F:319-357/Region: tetramer association
 F:779,12,18,23,37/Binding site: phosphate (Ser) (covalent) #status predicted
 F:173,176,235,239/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
 F:312/Binding site: phosphate (Ser) (covalent) (by cdc2 kinase) #status predicted

 Query Match 20.7%; Score 702; DB 2; Length 381;
 Best Local Similarity 41.3%; Pred. No. 3e-41;
 Matches 164; Conservative 69; Mismatches 114; Indels 50; Gaps 14;

 QY 14 TFEHLWSLEPDSYFDLPQSSRGNNVGGTSSMDVHLEGMTSYMAQFNLLSSTMD 73
 DB 21 TFSGLWKLPPPE----DILSPHCHMDLLLPQD--VEEF-FEGPSEAL----- 61

 QY 74 QMSRAASAPY--TPEHAASVTHSPYAPQSPSTFTMSPAPVPSNTDYPGPHFEVTF 131
 DB 62 RVSGAPAAQDPVETPGVPAPAPA--TPW--PLSSF-----VPSQTYQNGYFHLGF 110

 QY 132 QOSSTAKSATWYSPLLKLYCQIAKTCPIQIKVSTPPPPGTAIRAMPVYKAEHVTDV 191
 DB 111 LOSGTAKSVMTYSPPLNKLFCQIAKTCPIQVQVWVATPPAGSRVRAAIYKKSQHWTEV 170

 QY 192 KRCNHELGRDFNEGQASASHLIRVEGNLSQYVDDPTGQSVVYVPEPQVGTETFT 251
 DB 171 RCPHHERCSD-GDG-LAPQHLIRVEGNLYPEYLEDROTFRHSVYVPEPEAGSEYTT 228

 QY 252 ILYNFMNCSSCGVMNRRLIITILEMRDGOVLGRSFEGRICACPGDRKADSDHYRE 311
 DB 229 IHXYMNCSSCGVMNRRLIITILEDSGNLLGRDSFEVRVCAVCPGDRKADSDHYRE 288

 QY 312 QOALNESSAKNGAASKRAFKQSPVAPVAGVYKRRHGDDETYIYQVGRNFEILMKL 371
 DB 289 KEVLCPELPPGSA--KRALPTCTASAPP-----QKKKPLDGEYFTLKIRGRKRFEMFREL 341

QY 372 KESLELMELVQPLVDVSYQQOQLQRP-SHLQPPSY 407
 Db 342 NEALELK-----DAHATEESGDSRAHSSLLQPRAF 370

RESULT 13

cellular tumor antigen p53 - dog (fragment)
 C:Species: Canis lupus familiaris (dog)
 C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 05-May-2000
 C:Accession: I46226
 R:Devilee, P.; Van Leeuwen, I.S.; Voesten, A.; Rutteman, G.R.; Vos, J.H.; Cornelisse, C.
 Anticancer Res. 14, 2039-2046, 1994
 A:Title: The canine p53 gene is subject to somatic mutations in thypoid carcinoma.
 A:Reference number: I46226; MUID:95150524
 A:Accession: I46226
 A:Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: DNA
 A:Residues: 1-77 <DEV>
 A:Cross-references: GB:L27630; NID:9508454; PIDN:AAC37327.1; PID:g508455
 C:Genetics:
 A:Gene: p53
 A:Introns: 24/1; 51/3
 C:Superfamily: cellular tumor antigen p53

Query Match 7.3%; Score 248.5; DB 2; Length 77;
 Best Local Similarity 61.5%; Pred. No. 1.1e-10;
 Matches 48; Conservative 13; Mismatches 16; Indels 1; Gaps 1;

QY 183 KAEHTVDVKKCPNHELGRENFGQSQAPASHLIRVEGNLSQYDDPVTGQSVVVPYEP 242

Db 1 KSEFTEVVRCPHRCSDSDG-LAPQHLIRVEGNLRKAYLDDYTFRRHSVVVVPYEP 59

QY 243 PQVGTFTTILYNMCSN 260

Db 60 PEVGFDTYTHYNTMNS 77

RESULT 14

T00074
 hypothetical protein KIAA0460 - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 21-Jul-2000
 C:Accession: T00074
 R:Seiki, N.; Ohira, M.; Nagase, T.; Ishikawa, K.; Miyajima, N.; Nakajima, D.; Nomura, N.;
 DNA Res. 4, 345-349, 1997
 A:Title: Characterization of cDNA clones in size-fractionated cDNA libraries from human
 A:Reference number: Z14085; MUID:98116662
 A:Accession: T00074
 A:Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: mRNA
 A:Residues: 1-903 <SEK>
 A:Cross-references: EMBL:AB007929; NID:g3413881; PIDN:BA32305.1; PID:g3413882
 A:Experimental source: Brain
 C:Genetics:
 A:Note: KIAA0460

Query Match 4.5%; Score 151.5; DB 2; Length 903;
 Best Local Similarity 21.1%; Pred. No. 0.018;
 Matches 175; Conservative 75; Mismatches 253; Indels 327; Gaps 45;

QY 3 QSTATSPD-----GGTTTEHL-----WSSLEPSTYFDLPQSSRGNNVVGTD 46

Db 102 EESTSPSLEMKIHNFLKNGPGFSGNLNIPILSSLGSA-----PSESHPSDFQRGPTS 156

QY 47 SSMDFVLEGM-----TTSVMAQFNLLSSTWDQMSSRAASA-SP-- 84

Db 157 TSID-NIDGTPVDRSGTPTQDEMMDKPTSSVDVTSLLSKIIISGSSPSTSRGPP 214

QY 85 -----YTPHAASVPTH-----SPYAPQSPSTFTMSPAPVPSNT----- 119

Db 215 GRDESYPRELSNSVTRPRFGLASESPYKQPSDGM-E-RPSSLMDSSQEKYPTDTSFOED 272

QY 120 -----DYPGPHPEVTFQOSTAKSA-----TWYSPLLKKLYCOIAKTCPIQIKV 165
 Db 273 EDYRDFEYSGPPSAPMANLEKKKILKSSKLSDDTTEYQILSS-YSHRAQ--EFGYKS 329
 QY 166 STPPPGTATAMPYKKAHVTDVVKRP-----NHELGRD-----FN 204
 Db 330 AFPP-----SVRAL-----LDSSENCRLSSSPGLFGAFSVRGNPEGSRSPSKN 376
 QY 205 EGQAPASHLIRVEGNLS-----QYVDDP-----VTGQSVVVPY-BPP 243
 Db 377 DSFTPDPSN-----HNSLSQSTTGHLSPQKQYDPSPHVRHSLFSPQNTLAATGHP 431
 QY 244 QVGEFTTILYNMCSNCGVMN-----RRPILLIILEMRDQVGLRRSFEGRIC-- 295
 Db 432 TSGVE--KVLAISTTSTTEFNMLKNASRK-----SDDKHFGQAPSKTPTSDG 480
 QY 296 -----ACPGDRKADHDHYREQQA-----LNESSAKNGA-----ASKRAF 330
 Db 481 VLSNLTQPSLTATDQOQEEHYRIETRVSSCLDLPDSTEKGAPIETLGVHSASNRM 540
 QY 331 KQSP-----PAPALGAGYKRRGDEDT-----YLLQVRENFEEILMKLESLEL----- 377
 Db 541 SGEPIQTVESIRVPGK--NRGHGREASRVGWFDLSTSGSSFDNGPSSASELASLGSGGS 598
 QY 378 -----MELVP--QPLVDYSRQOQLQRP-SHLQ-----PSYGP 409
 Db 599 GGLTGFKTAPYKERAPQFQESVGSFRSNFSNTEFHEHLPPSPLEHCTPFQREPVGSSAP 658
 QY 410 VLSPNKVVHGM-----NKLPSVN-----QLVGQPPPHSSAANTNLGVPVGP 451
 Db 659 FVPP--KDHGIFGRDAPTHLPSVDLSNPFTEKAAHAAPPPPGEGHSGIFPTPPPP- 715
 QY 452 MLNHHGAVPANGSMSSSAQSMVSGSHCTPPPYHADPSLVSF-----LTGLGCPNCE 507
 Db 716 -----PPGHESS--SGSGVPFSTPPPPPPVHDGSHGVVPPAPPPLAEGVAGAYA 764
 QY 508 YFTSQGLQSIYH---LQNLTIEDLGALKIPEQYRMTWIRGLQDLKQGHYDYSTAQQLRSS 564
 Db 765 VFPKD-----HSSLQGLTAEHFGVLPGP-----RDHGGFTQ--RDL 799
 QY 565 NAATISIGSGELQQRVMEAVHFRVHTITPN-----RGPGGG 605
 Db 800 NGPGLS-----RVRESLTLPSSHLEHLGPHPGGGGG 831

RESULT 15

T19361
 hypothetical protein Cl7G1.4 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000
 C:Accession: T19361
 R:White, S.
 submitted to the EMBL Data Library, August 1996
 A:Reference number: Z19114
 A:Accession: T19361
 A:Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: DNA
 A:Residues: 1-925 <WIL>
 A:Cross-references: EMBL:Z78415; PIDN:CA01670.1; GSPDB:GN00028; CESP:Cl7G1.4
 A:Experimental source: clone Cl7G1
 C:Genetics:
 A:Gene: CESP:Cl7G1.4
 A:Map position: X
 C:Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homol-

Query Match 4.4%; Score 148.5; DB 2; Length 925;

Best Local Similarity 21.6%; Pred. No. 0.03;

Matches 135; Conservative 74; Mismatches 232; Indels 185; Gaps 32;

QY 4 STATSPDG-GTT-----FEHLWSLEPDSYFDLPQ-----SSRGNNV 42

Db 369 STPGTSGHGTGVSNAFLSHQKPSQOQSMHNLPHHQYNONNLLSPNIGASSLSQKQ 428

